Sequence of the *Trichoderma viride* phosphoglycerate kinase gene

Gustavo H.Goldman, Raimundo Villarroel, Marc Van Montagu* and Alfredo Herrera-Estrella
Laboratorium voor Genetica, Rijksuniversiteit Gent, K.L.Ledeganckstraat 35, B-9000 Gent, Belgium

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The *Trichoderma viride pgk* gene was isolated from a genomic library cloned in pT_3T_7lac using a synthetic oligonucleotide probe derived from the sequence of the *pgk* gene of *T. reesei* (1). Four clones were obtained and hybridized with 750-bp fragment of *T. reesei pgk*. Only one of the clones showed high homology using these hybridization conditions. We suggest, deduced from comparisons with other sequences of the *pgk* gene, that there are introns at nucleotide positions from 135 to 325 and from 747 to 819, respectively. The deduced amino acid sequence comparison showed a high homology with *pgk* from other species: 81% with *T. reesei* (1) and 55% with *Saccharomyces cerevisiae* (2).

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2. Hitzeman,R.A., Hagie,F.E., Hayflick,J.S., Chen,C.Y., Seeburg,P.H. and Derynck,R. (1982) *Nucl. Acids Res.* **23**, 7791–7808.

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-50  TCTTTTGCAGCGCGAGTCTTGTTTCGCTTACACGCCAGTATCCAGCCAAAATGTCTCTCTCCAACAAGCTGTCCATCACCGACGTCGACGTCAAGGGCAAG   51
                                                    M  S  L  S  N  K  L  S  I  T  D  V  D  V  K  G  K

 52  AGGGTCCTGATTCGGGTGAGTCCGGATTGCCCCGCCACTGCAGTGATGAAAAATGGAGGGGACCAAGTTGGGAGCTTTAGCATCGACGTCAAAGCTCTGCT   152
       R  V  L  I  R  V  S  P  D  C  P

153  AGAGGAGCGCCGTCGAGAAGGCTAATCTCTCGCTGGCTTTGGGCAATATGGGGATATTTGATAGCAGATGTCAGAAGCTTTGTTTGGTCGTATTTGGCTGA   253

254  CTGATGTGCTGTGTTTGTCCAGGTCGACTTCAACGTGCCCCTCGATGAGAACAAGAACATCACCAACCCCCAGCGAATTGCCGGTGCCATCCCCACCATCA   354
                         V  D  F  N  V  P  L  D  E  M  K  M  I  W  N  P  Q  R  I  A  G  A  I  P  T  I

355  AGCACGCTCTCGACAATGGCGCCAAGGCTGTCATCCTGATGTCCCACCTCGGACGTCCCAATGGCGCTGTCAACGCCAAGTACTCCCTCAAGCCTGTTGTT   455
       K  H  A  L  D  N  G  A  K  A  V  I  L  M  S  H  L  G  R  P  N  G  A  V  N  A  K  Y  S  L  K  P  V  V

456  CCCAAGCTGGAGGAGCTCCTTGGCAAGCCCGTCACCTTTGCTCCCGACTGTGTCGGCCCCGAGGTCGAGGCCATTGTCAACAAGGCCGACAACGGCGCTGT   556
       P  K  L  E  E  L  L  G  K  P  V  T  F  A  P  D  C  V  G  P  E  V  E  A  I  V  N  K  A  D  N  G  A  V

557  TATCCTGCTGGAGAACCTCCGATTCCACATTGAGGAGGAGGGCAGCTCCAAGGACAAGGAGGGCAACAAGACCAAGGCCGACAAGGCCAAGGTTGAGGAGT   657
         I  L  L  E  N  L  R  F  H  I  E  E  E  G  S  S  K  D  K  E  G  N  K  T  K  A  D  K  A  K  V  E  E

658  TCCGCAAGGGCCTGACTGCTCTGGGCGACGTTTACGTCAGTAAGTGCAATACTCTCTCTCGTCTGGAAAGCTGTTTTGTTTTTACATGTGGCTAATTTGTG   758
       F  R  K  G  L  T  A  L  G  D  V  Y  V

759  TCGCCAACTAGACGATGCTTTCGGCACTGCCCACCGTGCCCACTCTTCCATGGTTGGCGTTGACCTGCCCCAGAAGGCCGCCGGTTTCCTCATGAAGAAGG   859
               N  D  A  F  G  T  A  H  R  A  H  S  S  M  V  G  V  D  L  P  Q  K  A  A  G  F  L  M  K  K

860  AGCTCGACTACTTCGCCAAGGCTCTCGAGTCCCCTCAGCGACCCTTCCTTGCCATCCTCGGTGGCGCCAAGGTCTCTGACAAGATCCAGCTCATTGACAAC   960
       E  L  D  Y  F  A  K  A  L  E  S  P  Q  R  P  F  L  A  I  L  G  G  A  K  V  S  D  K  I  Q  L  I  D  N

961  CTGCTTGACAAGGTCAACACCCTCATCATCTGCGGTGGCATGGCTTTCACCTTCAAGAAGGTCCTGGACAACCTCGCCATTGGTGACTCTCTCTTCGACAA   1061
       L  L  D  K  V  N  T  L  I  I  C  G  G  M  A  F  T  F  K  K  V  L  D  N  L  A  I  G  D  S  L  F  D  K

1062  GGCCGGTGCCGAGACCGTTCCCAAGCTGGTTGAGAAGGCCAAGGCCAAGAACGTCAAGATTGTCCTGCCTACCGACTTCATCACCGCCGACAAGTTCGACA   1162
        A  G  A  E  T  V  P  K  L  V  E  K  A  K  A  K  N  V  K  I  V  L  P  T  D  F  I  T  A  D  K  F  D

1163  AGGACGCCAACACTGGCCTCGCCACTGACAAGGACGGCATCCCCGATGGATGGATGGGCCTCGACTGTGGTGACGAGTCCATCAAGCTGTACAAGGAGGCC   1263
       K  D  A  N  T  G  L  A  T  D  K  D  G  I  P  D  G  W  M  G  L  D  C  G  D  E  S  I  K  L  Y  K  E  A

1264  ATTGACGAGGCCAAGACCATCCTGTGGAACGGCCCTGCTGGTGTCTTTGAGTTTGAGAAGTTCGCTGGCGGCACCAAGGCCACCCTTGACGCTGTCGTCGA   1364
       I  D  E  A  K  T  I  L  W  N  G  P  A  G  V  F  E  F  E  K  F  A  G  G  T  K  A  T  L  D  A  V  V  E

1365  GGGCTGCAAGAACGGCAAGATTGTCATCATTGGCGGTGGTGACACTGCTACCGTCGCTGCCAAGTATGGCGTCGAGGATAAGCTGAGCCACGTCTCCACTG   1465
        G  C  K  N  G  K  I  V  I  I  G  G  G  D  T  A  T  V  A  A  K  Y  G  V  E  D  K  L  S  N  V  S  T

1466  GGTGGCGGTGCCAGCTTGGAGCTGTTGGAGGGCAAGGAGCTCCCCGGTGTCACTGCTCTGTCCAGTAAGTAAATTGCATACCCTACTTATGGGTCGAATGA   1566
       G  G  G  A  S  L  E  L  L  E  G  K  E  L  P  G  V  T  A  L  S  S  K

1567  GAGCGAGAGGAATAAATTGATGACGGGGGGATATGGCATAAAAAGGTCGGCTCGGAGCACCCCATTTTTAACGGAAAAAAGTATATAAACATATACCAGTG   1667
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* To whom correspondence should be addressed